

AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings of claims in the application.

Listing of claims

1. - 35. (Canceled)

36. (Currently amended) A method of identifying a human having an increased risk for developing positive autoantibody rheumatoid factor (RF+) Rheumatoid Arthritis (RA), comprising ~~determining the identity detecting the presence~~ of a single nucleotide polymorphism (SNP) in said human's nucleic acids as shown by at position 101 of SEQ ID NO: 5502 or its complement ~~thereof in said human's nucleic acids, wherein the presence of CG or its complement at the SNP position 101 of SEQ ID NO: 5502 or its complement thereof is~~ indicative of an increased risk for developing RF+ RA in said human.

37. - 38. (Canceled)

39. (Previously presented) The method of claim 36 in which SEQ ID NO: 5502 is contained within the genomic sequence of the TRIP gene as shown by SEQ ID NO: 1688.

40. (Currently amended) The method of claim 36 in which the SNP ~~to be detected is~~ located at position 6497 of SEQ ID NO: 1688.

41. (Currently amended) The method of claim 36 in which said human's nucleic acids are extracted from a biological sample of said human ~~therefrom~~.

42. (Previously presented) The method of claim 41 in which said biological sample is blood.

43. (Currently amended) The method of claim 36 in which said human's nucleic acids are amplified before the identity of the SNP is determined ~~detection is carried out~~.

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44. (Currently amended) The method of claim 36 in which the identity of the SNP is determined ~~detection is carried out~~ by using detection reagents comprising the nucleotide sequences of SEQ ID NO: 6629, SEQ ID NO: 6630, and SEQ ID NO: 6631.

45. (Currently amended) The method of claim 36 in which the identity of the SNP is determined ~~detection is carried out~~ by a process selected from the group consisting of: allele-specific probe hybridization, allele-specific primer extension, allele-specific amplification, sequencing, 5' nuclease digestion, molecular beacon assay, oligonucleotide ligation assay, size analysis, and single-stranded conformation polymorphism.

46. - 55. (Canceled)

56. (Currently amended) A method of determining a human's risk for developing positive autoantibody rheumatoid factor (RF+) Rheumatoid Arthritis (RA), comprising determining the identity of ~~detecting~~ a single nucleotide polymorphism (SNP) in said human's nucleic acids as shown by at position 101 of SEQ ID NO: 5502 or its complement thereof in said human's nucleic acids, wherein the presence of CG or its complement at the SNP position 101 of SEQ ID NO: 5502 or its complement thereof is indicative of an increased risk for RF+ RA in said human, or, the presence of T or its complement at the SNP position 101 of SEQ ID NO: 5502 or its complement thereof is indicative of a decreased risk for developing RF+ RA in said human.

57. - 58. (Canceled)

59. (Previously presented) The method of claim 56 in which SEQ ID NO: 5502 is contained within the genomic sequence of the TRIP gene as shown by SEQ ID NO: 1688.

60. (Currently amended) The method of claim 56 in which the SNP ~~to be detected~~ is located at position 6497 of SEQ ID NO: 1688.

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61. (Currently amended) The method of claim 56 in which said human's nucleic acids are extracted from a biological sample of said human ~~therefrom~~.
62. (Previously presented) The method of claim 61 in which said biological sample is blood.
63. (Currently amended) The method of claim 56 in which said human's nucleic acids are amplified before the identity of the SNP is determined ~~detection is carried out~~.
64. (Currently amended) The method of claim 56 in which the identity of the SNP is determined ~~detection is carried out~~ by using detection reagents comprising the nucleotide sequences of SEQ ID NO: 6629, SEQ ID NO: 6630, and SEQ ID NO: 6631.
65. (Currently amended) The method of claim 56 in which the identity of the SNP is determined ~~detection is carried out~~ by a process selected from the group consisting of: allele-specific probe hybridization, allele-specific primer extension, allele-specific amplification, sequencing, 5' nuclease digestion, molecular beacon assay, oligonucleotide ligation assay, size analysis, and single-stranded conformation polymorphism.
66. (Currently amended) A method of identifying a human having a decreased risk for developing positive autoantibody rheumatoid factor (RF+) Rheumatoid Arthritis (RA), comprising determining the identity ~~detecting the presence of~~ a single nucleotide polymorphism (SNP) in said human's nucleic acids as shown by ~~at~~ position 101 of SEQ ID NO: 5502 or its complement ~~thereof in said human's nucleic acids~~, wherein the presence of T or its complement ~~at the SNP position 101 of SEQ ID NO: 5502 or its complement thereof~~ is indicative of a decreased risk for RF+ RA in said human.
67. (Previously presented) The method of claim 66 in which SEQ ID NO: 5502 is contained within the genomic sequence of the TRIP gene as shown by SEQ ID NO: 1688.

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68. (Currently amended) The method of claim 66 in which the SNP ~~to be detected~~ is located at position 6497 of SEQ ID NO: 1688.

69. (Currently amended) The method of claim 66 in which said human's nucleic acids are extracted from a biological sample of said human therefrom.

70. (Previously presented) The method of claim 69 in which said biological sample is blood.

71. (Currently amended) The method of claim 66 in which said human's nucleic acids are amplified before the identity of the SNP is determined ~~detection is carried out~~.

72. (Currently amended) The method of claim 66 in which the identity of the SNP is determined ~~detection is carried out~~ by using detection reagents comprising the nucleotide sequences of SEQ ID NO: 6629, SEQ ID NO: 6630, and SEQ ID NO: 6631.

73. (Currently amended) The method of claim 66 in which the identity of the SNP is determined ~~detection is carried out~~ by a process selected from the group consisting of: allele-specific probe hybridization, allele-specific primer extension, allele-specific amplification, sequencing, 5' nuclease digestion, molecular beacon assay, oligonucleotide ligation assay, size analysis, and single-stranded conformation polymorphism.

74. (New) A method of identifying a human having a decreased risk for developing positive autoantibody rheumatoid factor (RF+) Rheumatoid Arthritis (RA), comprising determining the identity of the single nucleotide polymorphism (SNP) rs2276864 in said human's nucleic acids, wherein the presence of T or its complement at the SNP is indicative of a decreased risk for RF+ RA in said human.